



SEQUENCE LISTING

- <110> Sanders, Bob G.
Kline, Kimberly
Yu, Weiping
Liu, Hui
Hantash, Feras
- <120> Tocopherol Associated Protein and Uses Thereof
- <130> D6453CIP
- <140> US 10/696,699
<141> 2003-10-29
- <150> US 10/419,629
<151> 2003-04-21
- <160> 19
- <210> 1
<211> 1137
<212> DNA
<213> *Homo sapiens*
- <220>
<223> TAP-38 gene sequence

<400> 1

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tgtggagttc	cgaaagcaaa	aggacattga	caacatcatt	agcatggcag	150
cctccagagg	tgatccaaca	gtatctgtca	ctggatgcca	agggtctgct	200
gttctcagcc	tccaaacagg	acctgctgag	gaccaagatg	ctggatgcca	250
agggtctgct	gttctcagcc	tccaaacagg	acctgctgag	gaccaagatg	300
cgggagtggt	agctgcttct	gcaagagtgt	gccaccaga	ccacaaagtt	350
ggggaggaag	gtggagacca	tcaccataat	ttatgactgc	gaggggcttg	400
gcctcaagca	tctctggaag	cctgctgtgg	aggcctatgg	agagtttctc	450
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taaagcccc	aaactgtttc	ctgtggccta	taacctcatc	aaacccttcc	550
tgagtgagga	cactcgtaag	aagatcatgg	tcctgggagc	aaattggaag	600
gaggttttac	tgaaacatat	cagccctgac	caggtgcctg	tggagtatgg	650
gggcgccatg	actgaccctg	atggaaaccc	caagtgcaaa	tccaagatca	700
actacggggg	tgacatcccc	aggaagtatt	atgtgcgaga	ccaggtgaaa	750
cagcagtatg	aacacagcgt	gcagatttcc	cgtggctcct	cccaccaagt	800
ggagtatgag	atcctcttcc	ctggctgtgt	cctcaggtgg	cagtttatgt	850
cagatggagc	ggatgttggt	tttgggattt	tcctgaagac	caagatggga	900
gagaggcagc	gggcagggga	gatgacagag	gtgctgcca	accagaggta	950
caactcccac	ctggtccctg	aagatgggac	cctcacctgc	agtgatcctg	1000
gcattctatgt	cctgcggttt	gacaacacct	acagcttcat	tcatgccaaag	1050
aaggtcaatt	tcactgtgga	ggtcctgctt	ccagacaaag	cctcagaaga	1100

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1137

<210> 2
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 <212> PRT
 <213> *Homo sapiens*

<220>
 <221> PEPTIDE
 <223> TAP-38 polypeptide

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 Ser Gly Ser Met Trp Ser Ser Glu Ser Lys Arg Thr Leu Thr Thr
 35 40 45
 Ser Leu Ala Trp Gln Pro Pro Glu Val Ile Gln Gln Tyr Leu Ser
 50 55 60
 Gly Gly Met Cys Gly Tyr Asp Leu Asp Gly Cys Pro Val Trp Tyr
 65 70 75
 Asp Ile Ile Gly Pro Lys Asp Ala Lys Gly Leu Leu Phe Ser Ala
 80 85 90
 Ser Lys Gln Asp Leu Leu Arg Thr Lys Met Arg Glu Cys Glu Leu
 95 100 105
 Leu Leu Gln Glu Cys Ala His Gln Thr Thr Lys Leu Gly Arg Lys
 110 115 120
 Val Glu Thr Ile Thr Ile Ile Tyr Asp Cys Glu Gly Leu Gly Leu
 125 130 135
 Lys His Leu Trp Lys Pro Ala Val Glu Ala Tyr Gly Glu Phe Leu
 140 145 150
 Cys Met Phe Glu Glu Asn Tyr Pro Glu Thr Leu Lys Arg Leu Phe
 155 160 165
 Val Val Lys Ala Pro Lys Leu Phe Pro Val Ala Tyr Asn Leu Ile
 170 175 180
 Lys Pro Phe Leu Ser Glu Asp Thr Arg Lys Lys Ile Met Val Leu
 185 190 195
 Gly Ala Asn Tyr Lys Glu Val Leu Leu Lys His Ile Ser Pro Asp
 200 205 210
 Gln Val Pro Val Glu Tyr Gly Gly Thr Met Thr Asp Pro Asp Gly
 215 220 225
 Asn Pro Lys Cys Lys Ser Lys Ile Asn Tyr Gly Gly Asp Ile Pro
 230 235 240
 Arg Lys Tyr Tyr Val Arg Asp Gln Val Lys Gln Gln Tyr Glu His
 245 250 255
 Ser Val Gln Ile Ser Arg Gly Ser Ser His Gln Val Glu Tyr Glu
 260 265 270
 Ile Leu Phe Pro Gly Cys Val Leu Arg Trp Gln Phe Met Ser Asp
 275 280 285

Gly	Ala	Asp	Val	Gly	Phe	Gly	Ile	Phe	Leu	Lys	Thr	Lys	Met	Gly	
				290					295					300	
Glu	Arg	Gln	Arg	Ala	Gly	Glu	Met	Thr	Glu	Val	Leu	Pro	Asn	Gln	
				305					310					315	
Arg	Tyr	Asn	Ser	His	Leu	Val	Pro	Glu	Asp	Gly	Thr	Leu	Thr	Cys	
				320					325					330	
Ser	Asp	Pro	Gly	Ile	Tyr	Val	Leu	Arg	Phe	Asp	Asn	Thr	Tyr	Ser	
				335					340					345	
Phe	Ile	His	Ala	Lys	Lys	Val	Asn	Phe	Thr	Val	Glu	Val	Leu	Leu	
				350					355					360	
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Thr	Pro	Lys													

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 <213> *Homo sapiens*

<220>
 <223> TAP-46 gene sequence

<400> 3

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atgactatth	tctcctgcgt	tggctccgag	ccagaagctt	cgacctgcag	150
aagtcggagg	ccatgctccg	gaagcatgtg	gagttccgaa	agcaaaagga	200
cattgacaac	atcattagct	ggcagcctcc	agaggtgatc	caacagtatc	250
tgtcactgga	tgccaagggt	ctgctgttct	cagcctccaa	acaggacctg	300
ctgaggacca	agatgctgga	tgccaagggt	ctgctgttct	cagcctccaa	350
acaggacctg	ctgaggacca	agatgcggga	gtgtgagctg	cttctgcaag	400
agtgtgcccc	ccagaccaca	aagttgggga	ggaaggtgga	gaccatcacc	450
ataatttatg	actgcgaggg	gcttggcctc	aagcatctct	ggaagcctgc	500
tgtggaggcc	tatggagagt	ttctctgcat	gtttgaggaa	aattatcccc	550
aaacactgaa	gcgtcttttt	gttggttaaag	cccccaaact	gtttcctgtg	600
gcctataacc	tcatcaaacc	cttcctgagt	gaggacactc	gtaagaagat	650
catggtcctg	ggagcaaatt	ggaaggaggt	tttactgaaa	catatcagcc	700
ctgaccaggt	gcctgtggag	tatgggggcg	ccatgactga	ccctgatgga	750
aaccccaagt	gcaaatccaa	gatcaactac	gggggtgaca	tccccaggaa	800
gtattatgtg	cgagaccagg	tgaaacagca	gtatgaacac	agcgtgcaga	850
tttcccgtgg	ctcctcccac	caagtggagt	atgagatcct	cttccctggc	900
tgtgtcctca	ggtggcagtt	tatgtcagat	ggagcggatg	ttggtttttg	950
gattttcctg	aagaccaaga	tgggagagag	gcagcgggca	ggggagatga	1000
cagaggtgct	gccccaccag	aggtacaact	cccacctggg	ccctgaagat	1050
gggaccctca	cctgcagtga	tcctggcatc	tatgtcctgc	ggtttgacaa	1100
cacctacagc	ttcattcatg	ccaagaaggt	caatttcact	gtggagggtcc	1150
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accccgaaat	aa				1212

<210> 4
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 <212> PRT
 <213> *Homo sapiens*

<220>
 <221> PEPTIDE
 <223> TAP-46 polypeptide

<400> 4

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Pro	Asn	Pro	Asp	Asp	Tyr	Phe	Leu	Leu	Arg	Trp	Leu	Arg	Ala	Arg	35	40	45
Ser	Phe	Asp	Leu	Gln	Lys	Ser	Glu	Ala	Met	Leu	Arg	Lys	His	Val	50	55	60
Glu	Phe	Arg	Lys	Gln	Lys	Asp	Ile	Asp	Asn	Ile	Ile	Ser	Trp	Gln	65	70	75
Pro	Pro	Glu	Val	Ile	Gln	Gln	Tyr	Leu	Ser	Gly	Gly	Met	Cys	Gly	80	85	90
Tyr	Asp	Leu	Asp	Gly	Cys	Pro	Val	Trp	Tyr	Asp	Ile	Ile	Gly	Pro	95	100	105
Leu	Asp	Ala	Lys	Gly	Leu	Leu	Phe	Ser	Ala	Ser	Lys	Gln	Asp	Leu	110	115	120
Leu	Arg	Thr	Lys	Met	Arg	Glu	Cys	Glu	Leu	Leu	Leu	Gln	Glu	Cys	125	130	135
Ala	His	Gln	Thr	Thr	Lys	Leu	Gly	Arg	Lys	Val	Glu	Thr	Ile	Thr	140	145	150
Ile	Ile	Tyr	Asp	Cys	Glu	Gly	Leu	Gly	Leu	Lys	His	Leu	Trp	Lys	155	160	165
Pro	Ala	Val	Glu	Ala	Tyr	Gly	Glu	Phe	Leu	Cys	Met	Phe	Glu	Glu	170	175	180
Asn	Tyr	Pro	Glu	Thr	Leu	Lys	Arg	Leu	Phe	Val	Val	Lys	Ala	Pro	185	190	195
Lys	Leu	Phe	Pro	Val	Ala	Tyr	Asn	Leu	Ile	Lys	Pro	Phe	Leu	Ser	200	205	210
Glu	Asp	Thr	Arg	Lys	Lys	Ile	Met	Val	Leu	Gly	Ala	Asn	Trp	Lys	215	220	225
Glu	Val	Leu	Leu	Lys	His	Ile	Ser	Pro	Asp	Gln	Val	Pro	Val	Glu	230	235	240
Tyr	Gly	Gly	Thr	Met	Thr	Asp	Pro	Asp	Gly	Asn	Pro	Lys	Cys	Lys	245	250	255
Ser	Lys	Ile	Asn	Tyr	Gly	Gly	Asp	Ile	Pro	Arg	Lys	Tyr	Tyr	Val	260	265	270
Arg	Asp	Gln	Val	Lys	Gln	Gln	Tyr	Glu	His	Ser	Val	Gln	Ile	Ser	275	280	285
Arg	Gly	Ser	Ser	His	Gln	Val	Glu	Tyr	Glu	Ile	Leu	Phe	Pro	Gly	290	295	300
Cys	Val	Leu	Arg	Trp	Gln	Phe	Met	Ser	Asp	Gly	Ala	Asp	Val	Gly	305	310	315

Phe	Gly	Ile	Phe	Leu	Lys	Thr	Lys	Met	Gly	Glu	Arg	Gln	Arg	Ala	
				320					325					330	
Gly	Glu	Met	Thr	Glu	Val	Leu	Pro	Asn	Gln	Arg	Tyr	Asn	Ser	His	
				335					340					345	
Leu	Val	Pro	Glu	Asp	Gly	Thr	Leu	Thr	Cys	Ser	Asp	Pro	Gly	Ile	
				350					355					360	
Tyr	Val	Leu	Arg	Phe	Asp	Asn	Thr	Tyr	Ser	Phe	Ile	His	Ala	Lys	
				365					370					375	
Lys	Val	Asn	Phe	Thr	Val	Glu	Val	Leu	Leu	Pro	Asp	Lys	Ala	Ser	
				380					385					390	
Glu	Glu	Lys	Met	Lys	Gln	Leu	Gly	Ala	Gly	Thr	Pro	Lys			
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 <213> artificial sequence

<220>
 <221> primer_bind
 <223> TAP-38 sense oligonucleotide

<400> 5
 atgagcggca gagtcggcga t 21

<210> 6
 <211> 23
 <212> DNA
 <213> artificial sequence

<220>
 <221> primer_bind
 <223> TAP-38 antisense oligonucleotide

<400> 6
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<210> 7
 <211> 57
 <212> DNA
 <213> artificial sequence

<220>
 <221> primer_bind
 <223> TAP-38 sense oligonucleotide encoding HA-tag

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 cggcgat 57

<210> 8
 <211> 16
 <212> PRT
 <213> *Homo sapiens*
 <220>
 <221> PEPTIDE
 <223> 16 amino acids from the c-terminus of TAP attached
 to keyhole limpet hemocyanin

<400> 8
 Lys Ala Ser Glu Glu Lys Met Lys Gln Leu Gly Ala Gly Thr Pro
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 Lys

<210> 9
 <211> 27
 <212> DNA
 <213> artificial sequence

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 <223> sequence for an HA tag

<400> 9
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<210> 10
 <211> 59
 <212> DNA
 <213> artificial sequence

<220>
 <221> primer_bind
 <223> sense primer for the deletion mutant TAP-882

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 agcctccaa 59

<210> 11
 <211> 59
 <212> DNA
 <213> artificial sequence

<220>
 <221> primer_bind
 <223> sense primer for the deletion mutant TAP-681

<400> 11
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<210> 12
 <211> 59
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 <213> artificial sequence

<220>
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 caagatcaa 59

<210> 13
 <211> 21
 <212> DNA
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<220>
 <221> primer_bind
 <223> antisense primer for the TAP deletion mutants

<400> 13
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<210> 14
 <211> 882
 <212> DNA
 <213> *Homo sapiens*

<220>
 <223> deletion mutant TAP-882

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 gtgtgagctg cttctgcaag agtgtgcccc ccagaccaca aagttgggga 100
 ggaaggtgga gaccatcacc ataatttatg actgcgaggg gcttggcctc 150
 aagcatctct ggaagcctgc tgtggaggcc tatggagagt ttctctgcat 200
 gtttgaggaa aattatcccc aaacactgaa gcgtcttttt gttgttaaag 250
 cccccaaact gtttcctgtg gcctataacc tcatcaaacc cttcctgagt 300
 gaggacactc gtaagaagat catggtcctg ggagcaaatt ggaaggaggt 350
 tttactgaaa catatcagcc ctgaccaggt gcctgtggag tatgggggca 400
 ccatgactga ccctgatgga aaccccaagt gcaaattcaa gatcaactac 450
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 gtatgaacac agcgtgcaga tttcccgtgg ctctcccac caagtggagt 550

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gcagcgggca ggggagatga cagaggtgct gccaaccag aggtacaact 700
cccacctggc ccctgaagat gggaccctca cctgcagtga tcctggcatc 750
tatgtcctgc ggtttgacaa cacctacagc ttcattcatg ccaagaaggt 800
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<210>      15
<211>      293
<212>      PRT
<213>      Homo sapiens

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<220>
<221>      PEPTIDE
<223>      deletion mutant TAP-882

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Lys Leu Gly Arg Lys Val Glu Thr Ile Thr Ile Ile Tyr Asp Cys
                    35              40              45
Glu Gly Leu Gly Leu Lys His Leu Trp Lys Pro Ala Val Glu Ala
                    50              55              60
Tyr Gly Glu Phe Leu Cys Met Phe Glu Glu Asn Tyr Pro Glu Thr
                    65              70              75
Leu Lys Arg Leu Phe Val Val Lys Ala Pro Lys Leu Phe Pro Val
                    80              85              90
Ala Tyr Asn Leu Ile Lys Pro Phe Leu Ser Glu Asp Thr Arg Lys
                    95              100             105
Lys Ile Met Val Leu Gly Ala Asn Trp Lys Glu Val Leu Leu Lys
                    110             115             120
His Ile Ser Pro Asp Gln Val Pro Val Glu Tyr Gly Gly Thr Met
                    125             130             135
Thr Asp Pro Asp Gly Asn Pro Lys Cys Lys Ser Lys Ile Asn Tyr
                    140             145             150
Gly Gly Asp Ile Pro Arg Lys Tyr Tyr Val Arg Asp Gln Val Lys
                    155             160             165
Gln Gln Tyr Glu His Ser Val Gln Ile Ser Arg Gly Ser Ser His
                    170             175             180
Gln Val Glu Tyr Glu Ile Leu Phe Pro Gly Cys Val Leu Arg Trp
                    185             190             195
Gln Phe Met Ser Asp Gly Ala Asp Val Gly Phe Gly Ile Phe Leu
                    200             205             210
Lys Thr Lys Met Gly Glu Arg Gln Arg Ala Gly Glu Met Thr Glu
                    215             220             225
Val Leu Pro Asn Gln Arg Tyr Asn Ser His Leu Val Pro Glu Asp
                    230             235             240

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Gly	Thr	Leu	Thr	Cys	Ser	Asp	Pro	Gly	Ile	Tyr	Val	Leu	Arg	Phe	
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Asp	Asn	Thr	Tyr	Ser	Phe	Ile	His	Ala	Lys	Lys	Val	Asn	Phe	Thr	
				260					265					270	
Val	Glu	Val	Leu	Leu	Pro	Asp	Lys	Ala	Ser	Glu	Glu	Lys	Met	Lys	
				275					280					285	
Gln	Leu	Gly	Ala	Gly	Thr	Pro	Lys								
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<210> 16
 <211> 681
 <212> DNA
 <213> *Homo sapiens*

<220>
 <223> deletion mutant TAP-681

<400> 16

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aggacactcg	taagaagatc	atggctcctgg	gagcaaattg	gaaggaggtt	150
ttactgaaac	atatcagccc	tgaccaggtg	cctgtggagt	atggggggcac	200
catgactgac	cctgatggaa	accccaagtg	caaatccaag	atcaactacg	250
ggggtgacat	ccccaggaag	tattatgtgc	gagaccaggt	gaaacagcag	300
tatgaacaca	gcgtgcagat	ttcccgtggc	tcctcccacc	aagtggagta	350
tgagatcctc	ttccctggct	gtgtcctcag	gtggcagttt	atgtcagatg	400
gagcggatgt	tggttttggg	attttcctga	agaccaagat	gggagagagg	450
cagcgggcag	gggagatgac	agaggtgctg	cccaaccaga	ggtacaactc	500
ccacctggtc	cctgaagatg	ggaccctcac	ctgcagtgat	cctggcatct	550
atgtcctgcg	gtttgacaac	acctacagct	tcattcatgc	caagaaggtc	600
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<210> 17
 <211> 226
 <212> PRT
 <213> *Homo sapiens*

<220>
 <221> PEPTIDE
 <223> deletion mutant TAP-681

<400> 17

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Lys	Ala	Pro	Lys	Leu	Phe	Pro	Val	Ala	Tyr	Asn	Leu	Ile	Lys	Pro	
			20						25					30	
Phe	Leu	Ser	Glu	Asp	Thr	Arg	Lys	Lys	Ile	Met	Val	Leu	Gly	Ala	
			35						40					45	

Asn	Trp	Lys	Glu	Val	Leu	Leu	Lys	His	Ile	Ser	Pro	Asp	Gln	Val	
				50					55					60	
Pro	Val	Glu	Tyr	Gly	Gly	Thr	Met	Thr	Asp	Pro	Asp	Gly	Asn	Pro	
				65					70					75	
Lys	Cys	Lys	Ser	Lys	Ile	Asn	Tyr	Gly	Gly	Asp	Ile	Pro	Arg	Lys	
				80					85					90	
Tyr	Tyr	Val	Arg	Asp	Gln	Val	Lys	Gln	Gln	Tyr	Glu	His	Ser	Val	
				95					100					105	
Gln	Ile	Ser	Arg	Gly	Ser	Ser	His	Gln	Val	Glu	Tyr	Glu	Ile	Leu	
				110					115					120	
Phe	Pro	Gly	Cys	Val	Leu	Arg	Trp	Gln	Phe	Met	Ser	Asp	Gly	Ala	
				125					130					135	
Asp	Val	Gly	Phe	Gly	Ile	Phe	Leu	Lys	Thr	Lys	Met	Gly	Glu	Arg	
				140					145					150	
Gln	Arg	Ala	Gly	Glu	Met	Thr	Glu	Val	Leu	Pro	Asn	Gln	Arg	Tyr	
				155					160					165	
Asn	Ser	His	Leu	Val	Pro	Glu	Asp	Gly	Thr	Leu	Thr	Cys	Ser	Asp	
				170					175					180	
Pro	Gly	Ile	Tyr	Val	Leu	Arg	Phe	Asp	Asn	Thr	Tyr	Ser	Phe	Ile	
				185					190					195	
His	Ala	Lys	Lys	Val	Asn	Phe	Thr	Val	Glu	Val	Leu	Leu	Pro	Asp	
				200					205					210	
Lys	Ala	Ser	Glu	Glu	Lys	Met	Lys	Gln	Leu	Gly	Ala	Gly	Thr	Pro	
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Lys

<210> 18
 <211> 456
 <212> DNA
 <213> *Homo sapiens*

<220>
 <223> deletion mutant TAP-456

<400> 18

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gtggctcct	c	ccaccaagtg	gagtatgaga	tcctcttccc	tggtgtgtgc	150
ctcaggtggc	c	agtttatgtc	agatggagcg	gatgttggtt	ttgggattttt	200
cctgaagacc	c	aagatggggag	agaggcagcg	ggcagggggag	atgacagagg	250
tgctgccc	aa	ccagaggtac	aactcccacc	tggtccctga	agatggggacc	300
ctcacctgca	c	gtgatcctgg	catctatgtc	ctgcggtttg	acaacaccta	350
cagcttcatt	c	catgccaaga	aggtcaattt	cactgtggag	gtcctgcttc	400
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aaataa						456

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 <212> PRT
 <213> *Homo sapiens*

<220>

<221> PEPTIDE

<223> deletion mutant TAP-456

<400> 19

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Tyr	Tyr	Val	Arg	Asp	Gln	Val	Lys	Gln	Gln	Tyr	Glu	His	Ser	Val	
				20					25					30	
Gln	Ile	Ser	Arg	Gly	Ser	Ser	His	Gln	Val	Glu	Tyr	Glu	Ile	Leu	
				35					40					45	
Phe	Pro	Gly	Cys	Val	Leu	Arg	Trp	Gln	Phe	Met	Ser	Asp	Gly	Ala	
				50					55					60	
Asp	Val	Gly	Phe	Gly	Ile	Phe	Leu	Lys	Thr	Lys	Met	Gly	Glu	Arg	
				65					70					75	
Gln	Arg	Ala	Gly	Glu	Met	Thr	Glu	Val	Leu	Pro	Asn	Gln	Arg	Tyr	
				80					85					90	
Asn	Ser	His	Leu	Val	Pro	Glu	Asp	Gly	Thr	Leu	Thr	Cys	Ser	Asp	
				95					100					105	
Pro	Gly	Ile	Tyr	Val	Leu	Arg	Phe	Asp	Asn	Thr	Tyr	Ser	Phe	Ile	
				110					115					120	
His	Ala	Lys	Lys	Val	Asn	Phe	Thr	Val	Glu	Val	Leu	Leu	Pro	Asp	
				125					130					135	
Lys	Ala	Ser	Glu	Glu	Lys	Met	Lys	Gln	Leu	Gly	Ala	Gly	Thr	Pro	
				140					145					150	
Lys															